

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/534,279
Source: PCT
Date Processed by STIC: 05/23/2006

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 05/23/2006
 PATENT APPLICATION: US/10/534,279 TIME: 14:03:58

Input Set : A:\60290-USA Sequence Listing.txt
 Output Set: N:\CRF4\05232006\J534279.raw

3 <110> APPLICANT: Wu, Shilan
 4 Hayashi, Jon H.
 5 Kinne, Lyle P.
 6 Dierks, Peter M.
 8 <120> TITLE OF INVENTION: Lepidoptera Voltage-Gated Calcium Channels
 10 <130> FILE REFERENCE: FMC 60290
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/534,279
 C--> 12 <141> CURRENT FILING DATE: 2005-05-06
 12 <160> NUMBER OF SEQ ID NOS: 83
 14 <170> SOFTWARE: PatentIn version 3.2
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 5047
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Heliothis virescens
 21 <400> SEQUENCE: 1
 22 ggttggcgcc agcgcaggag gcggcgaaaa cgcaggctcg cgcggcgcca gctgatacc 60
 24 tggcgccgc gcaccagccc gctactccag ggcccagctc actctttata tttgcgcacg 120
 26 aaaatcctat tcggaggtaa acaaagttca tcatcgatg gccgccttc gagtacgcgg 180
 28 tgctgcttac catcatcgcc aactgcgtgg tgctggcgct ggaggagcat ttgcctaacg 240
 30 gcgataagac catcttagca cagaatctgg aaaagaccga ggcgtacttt ttaggaatat 300
 32 tttgtgtaga agcctcgataaa aaaatcttag ccttaggttt tttttacac aggggatcgt 360
 34 atcttaggaa cgttggAAC atcatggatt ttttgcgtgt agtaactggg atcatcacgc 420
 36 agctgccat cgcgcagcc gacgtcgact tcaggacctt ggcgtccatt aggggtgctga 480
 38 ggcccttaa attagtatcg ggcgttccta gtctgcaagt ggtactgaag tccatcataa 540
 40 aggcgatggc gccgttgcgtcagatcgcc tcctggctt tttcgacata gtcatctcg 600
 42 ctatcatcggtt cctcgatgtc tactcagggg cgctgcataa gactgttat aatttagaa 660
 44 atatttagtga aatagtaaat gaaggcgata gtgcgacgccc gtgtAACCGC gacaacgtga 720
 46 gtttagcacc atttggggca aacgtgtgtg attatgagaa gagcacgtgt ttagagaaat 780
 48 gggagggggc gaacagggtt attacgtcc tcgacaaat cggcttcgct atgctcacccg 840
 50 tctccatgt cattaccatg gagggctggc cgcacatctt ctattggacg aatgacgcgc 900
 52 taggtatgtc gttcaacttgg atttacttttgcgttcat agtattgggt tcattttta 960
 54 tgctcaactt agttctcggt gtccttagcg gtgagttcgc taaaagaaaaga gagaagat 1020
 56 aaaatagaca agaatttctt aaattaagaa gacagcagca actcgagaga gaactcaatg 1080
 58 gttacgttga gtggattttgtaa agcagagg aagtaatatt agcagaagaa agaacaacag 1140
 60 aagaagaaaa aatgcacata atagaagcac ggagaagagc agcggccaaa aagaagttaa 1200
 62 aaaaccttgg taaaagtaaa agcacagata cagaagagga agaacaagat gaagactgcg 1260
 64 gtgatgacgg ttttctaaaa agcaaagctc ggtcagccgg gaggtttgcgt gacttctggc 1320
 66 gggctgagaa gaggttccgg ttttggatca ggcacacagt gaagacccag tggttctact 1380
 68 ggttcgatcat tgcgttggcgt ctctcaaca cgatatgcgt cgctgttagag cattatagac 1440
 70 aacccaagtgcgtacttcgt tttttataact atgccaatttgcgttgcgttca 1500
 72 tgatggagat gtgggtgaag atgtatgcgc ttggccgcgt aatctacttc gactcgcc 1560
 74 tcaaccgggtt cgactgcgtg gtcatctccg gtcacatctt cgaggtcggt tggctcgagg 1620
 76 tcaagggtgg ctccctcggt ctatctgtcc tgagagctct aagactgttg aggatattta 1680

(PQ-6)

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| | | | | | | | |
|-----|-------------|-------------|-------------|-------------|--------------|-------------|------|
| 78 | aggtcaccaa | gtactggtca | tcgctccgga | acctggtgat | atctctcctc | aactcaatga | 1740 |
| 80 | gatccatcat | ctcgctgctg | ttcctgctct | tcctgttcat | tctcatcttc | gcactgctcg | 1800 |
| 82 | gcatgcagct | gttcggggga | cagttcaact | tcgaggacgg | cacgcccgg | accaacttca | 1860 |
| 84 | acacccttcc | tatcgcggtt | ttaactgtct | tccagatcct | aacaggtgaa | gattggaaacg | 1920 |
| 86 | aagtgtatgt | tgacggcatc | cagtcacagg | gcggcatcca | gagaggcatg | atctactctc | 1980 |
| 88 | tatactttgt | catcctcgtc | ttatggca | actacacgct | gctgaacgtg | ttccttgcta | 2040 |
| 90 | tcgctgtcga | caacttgct | aacgcccagg | aattgacggc | ggcagaagag | gaacaagtgc | 2100 |
| 92 | aggaggacaa | ggagaaacag | ctccaggaat | tggagaaagg | gatgggtgca | ttacacgcgg | 2160 |
| 94 | tggacggcac | tccaccggga | gtagatctaa | gtccctcttc | gccgacgagt | aggaagaaca | 2220 |
| 96 | aaaagaaaaga | agaggccaaa | aaagaagatg | aagatgaggt | accagatgga | ccaaaaccaa | 2280 |
| 98 | tgctgccata | ttcgtccatg | tttattttgt | cacctactaa | tccaaattagg | cgaggcgac | 2340 |
| 100 | actgggttgt | aaatthaaga | tattttattt | tttttatcat | ggtagttata | tgtatgagtt | 2400 |
| 102 | ctgcggcttt | agcggctgaa | gaccccgtag | tggagagag | tgacaggaac | aaaatcctga | 2460 |
| 104 | actacttoga | ttacgcgttc | acgggcgtgt | tcaccgtgga | gatgctgctg | aagatagtgg | 2520 |
| 106 | acctcgccat | cctgttccac | cggggcgcct | acctgcgcga | cctgtggaaac | atcatggatg | 2580 |
| 108 | ccggcgtcg | catatgcgcc | cttgcagct | tcggatttga | gatcgaggc | gtgaaaaagg | 2640 |
| 110 | gggcggggca | gaatctgtcc | acaataaaat | cgttaagagt | gttacgagtg | ctcagacctt | 2700 |
| 112 | tgaaaactat | aaaacgagtt | ccaaagttaa | aagcagtgtt | tgactgtgtt | gtgaactctt | 2760 |
| 114 | tgaaaaacgt | cattaacatt | ctcattgtgt | acatattgtt | tcaattcata | ttcgctgtaa | 2820 |
| 116 | ttgcagttca | acttttaat | ggtaaatttt | ttcactgcaa | cgatatcagt | aagaatactt | 2880 |
| 118 | ttgaagactg | ccaagggtcg | tatttcgtgt | acgagtcaaa | cagttgctg | ccgaaagtca | 2940 |
| 120 | accagcgcac | gtggacgacg | caatccttcc | attacgacaa | cgtcgccgtg | gctatgctta | 3000 |
| 122 | cgctgttcgc | cgtcagact | ggggaggggt | ggccacaagt | attacaaaat | tcaatggccg | 3060 |
| 124 | ccacctacga | agacagggga | cccatacaaa | atttcgaat | agaaatgtcc | atattttata | 3120 |
| 126 | tagttactt | cgtgggtttt | cctttcttct | ttgttaacat | attcgttagct | ctgataattt | 3180 |
| 128 | tcacatttca | agagcagggc | gaagctgagc | ttcaggatgg | tggaaatttgc | aagaatcaga | 3240 |
| 130 | aatcgtgtat | agacttcacg | atagaagcgc | gacctctcga | gaggatata | ccaaagcaaaa | 3300 |
| 132 | gggcgagttt | taagtacaaa | gtgtggagaa | tagttgtc | tacgccccttc | gagttacttca | 3360 |
| 134 | tcatgacgt | gatcgcttc | aacacattgt | tgctcatgt | gaagttcac | gaggctccac | 3420 |
| 136 | cactactcat | ggacatattt | acattcatga | acctcgctt | tacgaccttc | ttccttc | 3480 |
| 138 | agaccgtatt | gaagctgatc | gccttcgggt | gtacgaattt | tttcaaagac | ccttggaaata | 3540 |
| 140 | cattcgattt | tattacggtc | atttgcgtt | ttatttgc | ccttcattatg | gagttggcg | 3600 |
| 142 | agaacacatt | caacgtcggt | ttccttcgccc | tgttccggc | cgcgcgactg | atcaagctgc | 3660 |
| 144 | tccgacaggg | ctacactatt | cgatgactgc | tctggacatt | cgtgcagagt | ttcaaaagcct | 3720 |
| 146 | taccctacgt | gtgccttc | atcgatgc | tatttc | ctacgcccattc | atcggtatgc | 3780 |
| 148 | aggtgtttgg | caatataaaaa | ttaacaccag | agtctgacat | gaacagacac | aacaattttc | 3840 |
| 150 | gaagcttcat | tcaagcactc | atgctactgt | tcagatgcgc | aacggggcag | tcgtggccca | 3900 |
| 152 | acataatgtt | ggcttgcgc | aaacccgcca | agtgcgacat | agcagctgg | aaggcctcca | 3960 |
| 154 | acgaagaatg | tggaaatgt | ctcgctacg | cctacttcgt | atctttata | ttcttctgtt | 4020 |
| 156 | cgtttcttat | gttgaatttgc | ttcgttgc | ttattatgg | taactttgac | tacctaacga | 4080 |
| 158 | gggactcg | catttcggc | gcacatcattc | ttgatgaaatt | tgttagaata | tgggagaata | 4140 |
| 160 | atgatccaaa | cgccacgggt | aagatccatt | atacagaaat | gtatgatata | ttgaagaata | 4200 |
| 162 | tggatccgc | tctgggtttt | ggtaacaaat | gtccaaatag | actagcatat | aagaagctt | 4260 |
| 164 | ttagaatgaa | tatgcgccta | gacgatgagg | ggaaagttaa | ttttacaaca | acactatttgc | 4320 |
| 166 | ccttaatacg | agaaaaacttg | aacatcaaaa | tgagatctcc | cgaggaaatg | gaccaagcag | 4380 |
| 168 | atgaggaattt | aaggaaaca | ataacccaca | tttggccatt | acaagcgaag | aagatgctcg | 4440 |
| 170 | acctgctgtt | gcctcgaaac | gatgtactca | acgctggaaa | actgaccgtc | ggaaagatata | 4500 |
| 172 | acgctggact | tctaatcctc | gagagttgga | gatctacaag | gttcaagcag | aatgggttcc | 4560 |
| 174 | cggtaactgga | actacaagga | tcacaccacg | cctcaatgg | gtcggtggac | gagggacgg | 4620 |

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Input Set : A:\60290-USA Sequence Listing.txt
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176 tacaagctcc tcacacgtac cagaatggac accaccatgg gagatcatcc agtttaagac 4680
 178 gaacgcccag tccaagaaga cgaggccact acggaggtta tcatacgat atcggattct 4740
 180 cagacacccgt cagcaacgtc gtcgagatag taaagcatga acaccagaga cacggcgaa 4800
 182 cgcacagagc gccccactac taccacccac atgtttggc cccgataggt gagcgggagc 4860
 184 gggaccgcga gtggcgggag tggcgcgacc gctcctggg a g c g c g a g g g c g c g 4920
 186 gccgcggccg ccagttgccc cccacgccc a c a g g c g t c a c g t a c a g g t c a g c 4980
 188 agccacccat caccagaatc agccacagcc cctcacactt atcgctaagg cacaccgtca 5040
 190 gagaacc 5047
 193 <210> SEQ ID NO: 2
 194 <211> LENGTH: 1662
 195 <212> TYPE: PRT
 196 <213> ORGANISM: Heliothis virescens
 198 <400> SEQUENCE: 2
 200 Met Gly Gly Ala His Gln Pro Ala Thr Pro Gly Pro Ser Ser Leu Phe
 201 1 5 10 15
 204 Ile Phe Ala Asp Glu Asn Pro Ile Arg Arg Tyr Thr Lys Phe Ile Ile
 205 20 25 30
 208 Glu Trp Pro Pro Phe Glu Tyr Ala Val Leu Leu Thr Ile Ile Ala Asn
 209 35 40 45
 212 Cys Val Val Leu Ala Leu Glu Glu His Leu Pro Asn Gly Asp Lys Thr
 213 50 55 60
 216 Ile Leu Ala Gln Asn Leu Glu Lys Thr Glu Ala Tyr Phe Leu Gly Ile
 217 65 70 75 80
 220 Phe Cys Val Glu Ala Ser Leu Lys Ile Leu Ala Leu Gly Phe Val Leu
 221 85 90 95
 224 His Arg Gly Ser Tyr Leu Arg Asn Val Trp Asn Ile Met Asp Phe Phe
 225 100 105 110
 228 Val Val Val Thr Gly Ile Ile Thr Gln Leu Pro Ile Ala Pro Ala Asp
 229 115 120 125
 232 Val Asp Phe Arg Thr Leu Arg Ala Ile Arg Val Leu Arg Pro Leu Lys
 233 130 135 140
 236 Leu Val Ser Gly Val Pro Ser Leu Gln Val Val Leu Lys Ser Ile Ile
 237 145 150 155 160
 240 Lys Ala Met Ala Pro Leu Leu Gln Ile Gly Leu Leu Val Leu Phe Ala
 241 165 170 175
 244 Ile Val Ile Phe Ala Ile Ile Gly Leu Glu Phe Tyr Ser Gly Ala Leu
 245 180 185 190
 248 His Lys Thr Cys Tyr Asn Leu Glu Asp Ile Ser Glu Ile Val Asn Glu
 249 195 200 205
 252 Gly Asp Ser Ala Thr Pro Cys Asn Ala Asp Asn Val Ser Leu Ala Pro
 253 210 215 220
 256 Phe Gly Ala Asn Val Cys Asp Tyr Glu Lys Ser Thr Cys Leu Glu Lys
 257 225 230 235 240
 260 Trp Glu Gly Pro Asn Arg Gly Ile Thr Ser Phe Asp Asn Ile Gly Phe
 261 245 250 255
 264 Ala Met Leu Thr Val Phe Gln Cys Ile Thr Met Glu Gly Trp Thr Ala
 265 260 265 270
 268 Ile Leu Tyr Trp Thr Asn Asp Ala Leu Gly Ser Ala Phe Asn Trp Ile
 269 275 280 285

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Input Set : A:\60290-USA Sequence Listing.txt
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272 Tyr Phe Val Pro Leu Ile Val Leu Gly Ser Phe Phe Met Leu Asn Leu
 273 290 295 300
 276 Val Leu Gly Val Leu Ser Gly Glu Phe Ala Lys Glu Arg Glu Lys Val
 277 305 310 315 320
 280 Glu Asn Arg Gln Glu Phe Leu Lys Leu Arg Arg Gln Gln Gln Leu Glu
 281 325 330 335
 284 Arg Glu Leu Asn Gly Tyr Val Glu Trp Ile Cys Lys Ala Glu Glu Val
 285 340 345 350
 288 Ile Leu Ala Glu Glu Arg Thr Thr Glu Glu Glu Lys Met His Ile Ile
 289 355 360 365
 292 Glu Ala Arg Arg Ala Ala Ala Lys Lys Lys Leu Lys Asn Leu Gly
 293 370 375 380
 296 Lys Ser Lys Ser Thr Asp Thr Glu Glu Glu Gln Asp Glu Asp Cys
 297 385 390 395 400
 300 Gly Asp Asp Gly Phe Leu Lys Ser Lys Ala Arg Ser Ala Gly Arg Phe
 301 405 410 415
 304 Ala Asp Phe Trp Arg Ala Glu Lys Arg Phe Arg Phe Trp Ile Arg His
 305 420 425 430
 308 Thr Val Lys Thr Gln Trp Phe Tyr Trp Phe Val Ile Val Leu Val Leu
 309 435 440 445
 312 Phe Asn Thr Ile Cys Val Ala Val Glu His Tyr Arg Gln Pro Lys Trp
 313 450 455 460
 316 Leu Thr Ser Phe Leu Tyr Tyr Ala Glu Phe Val Phe Leu Gly Leu Phe
 317 465 470 475 480
 320 Met Met Glu Met Trp Val Lys Met Tyr Ala Leu Gly Pro Arg Ile Tyr
 321 485 490 495
 324 Phe Glu Ser Ser Phe Asn Arg Phe Asp Cys Val Val Ile Ser Gly Ser
 325 500 505 510
 328 Ile Phe Glu Val Val Trp Ser Glu Val Lys Gly Gly Ser Phe Gly Leu
 329 515 520 525
 332 Ser Val Leu Arg Ala Leu Arg Leu Leu Arg Ile Phe Lys Val Thr Lys
 333 530 535 540
 336 Tyr Trp Ser Ser Leu Arg Asn Leu Val Ile Ser Leu Leu Asn Ser Met
 337 545 550 555 560
 340 Arg Ser Ile Ile Ser Leu Leu Phe Leu Leu Phe Leu Phe Ile Leu Ile
 341 565 570 575
 344 Phe Ala Leu Leu Gly Met Gln Leu Phe Gly Gly Gln Phe Asn Phe Glu
 345 580 585 590
 348 Asp Gly Thr Pro Pro Thr Asn Phe Asn Thr Phe Pro Ile Ala Leu Leu
 349 595 600 605
 352 Thr Val Phe Gln Ile Leu Thr Gly Glu Asp Trp Asn Glu Val Met Tyr
 353 610 615 620
 356 Asp Gly Ile Gln Ser Gln Gly Gly Ile Gln Arg Gly Met Ile Tyr Ser
 357 625 630 635 640
 360 Leu Tyr Phe Val Ile Leu Val Leu Phe Gly Asn Tyr Thr Leu Leu Asn
 361 645 650 655
 364 Val Phe Leu Ala Ile Ala Val Asp Asn Leu Ala Asn Ala Gln Glu Leu
 365 660 665 670
 368 Thr Ala Ala Glu Glu Gln Val Glu Glu Asp Lys Glu Lys Gln Leu

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| | | | | | | | | | | | | | | | | | |
|-----|------|------|-----|-----|------|------|-----|-----|-----|-----|-----|-----|------|-----|------|-----|--|
| 369 | 675 | 680 | 685 | | | | | | | | | | | | | | |
| 372 | Gln | Glu | Leu | Glu | Lys | Gly | Met | Gly | Ala | Leu | His | Ala | Val | Asp | Gly | Thr | |
| 373 | 690 | | 695 | | 700 | | | | | | | | | | | | |
| 376 | Pro | Pro | Gly | Val | Asp | Leu | Ser | Pro | Ser | Ser | Pro | Thr | Ser | Arg | Lys | Asn | |
| 377 | 705 | | 710 | | 715 | | | | | | | | | | | 720 | |
| 380 | Lys | Lys | Glu | Glu | Ala | Lys | Lys | Glu | Asp | Glu | Asp | Glu | Val | Pro | Asp | | |
| 381 | | | | | | | | | | | | | | | 735 | | |
| 384 | Gly | Pro | Lys | Pro | Met | Leu | Pro | Tyr | Ser | Ser | Met | Phe | Ile | Leu | Ser | Pro | |
| 385 | | | | | | | | | | | | | | | 750 | | |
| 388 | Thr | Asn | Pro | Ile | Arg | Arg | Gly | Ala | His | Trp | Val | Val | Asn | Leu | Arg | Tyr | |
| 389 | | | | | | | | | | | | | | | 765 | | |
| 392 | Phe | Asp | Phe | Phe | Ile | Met | Val | Val | Ile | Cys | Met | Ser | Ser | Ala | Ala | Leu | |
| 393 | | | | | | | | | | | | | | | 780 | | |
| 396 | Ala | Ala | Glu | Asp | Pro | Val | Val | Glu | Glu | Ser | Asp | Arg | Asn | Lys | Ile | Leu | |
| 397 | 785 | | 790 | | 795 | | | | | | | | | | 800 | | |
| 400 | Asn | Tyr | Phe | Asp | Tyr | Ala | Phe | Thr | Gly | Val | Phe | Thr | Val | Glu | Met | Leu | |
| 401 | | | | | | | | | | | | | | | 815 | | |
| 404 | Leu | Lys | Ile | Val | Asp | Leu | Gly | Ile | Leu | Phe | His | Pro | Gly | Ala | Tyr | Leu | |
| 405 | | | | | | | | | | | | | | | 830 | | |
| 408 | Arg | Asp | Leu | Trp | Asn | Ile | Met | Asp | Ala | Ala | Val | Val | Ile | Cys | Ala | Leu | |
| 409 | | | | | | | | | | | | | | | 845 | | |
| 412 | Val | Ser | Phe | Phe | Glu | Ile | Gly | Gly | Val | Lys | Lys | Gly | Ala | Gly | Gln | | |
| 413 | | | | | | | | | | | | | | | 860 | | |
| 416 | Asn | Leu | Ser | Thr | Ile | Lys | Ser | Leu | Arg | Val | Leu | Arg | Val | Leu | Arg | Pro | |
| 417 | 865 | | 870 | | 875 | | | | | | | | | | 880 | | |
| 420 | Leu | Lys | Thr | Ile | Lys | Arg | Val | Pro | Lys | Leu | Lys | Ala | Val | Phe | Asp | Cys | |
| 421 | | | | | | | | | | | | | | | 895 | | |
| 424 | Val | Val | Asn | Ser | Leu | Lys | Asn | Val | Ile | Asn | Ile | Leu | Ile | Val | Tyr | Ile | |
| 425 | | | | | | | | | | | | | | | 910 | | |
| 428 | Leu | Phe | Gln | Phe | Ile | Phe | Ala | Val | Ile | Ala | Val | Gln | Leu | Phe | Asn | Gly | |
| 429 | | | | | | | | | | | | | | | 925 | | |
| 432 | Lys | Phe | Phe | His | Cys | Asn | Asp | Ile | Ser | Lys | Asn | Thr | Phe | Glu | Asp | Cys | |
| 433 | | | | | | | | | | | | | | | 940 | | |
| 436 | Gln | Gly | Ser | Tyr | Phe | Val | Tyr | Glu | Ser | Asn | Ser | Leu | Leu | Pro | Lys | Val | |
| 437 | 945 | | 950 | | 955 | | | | | | | | | | 960 | | |
| 440 | Asn | Gln | Arg | Thr | Trp | Thr | Thr | Gln | Ser | Phe | His | Tyr | Asp | Asn | Val | Ala | |
| 441 | | | | | | | | | | | | | | | 975 | | |
| 444 | Val | Ala | Met | Leu | Thr | Leu | Phe | Ala | Val | Gln | Thr | Gly | Glu | Gly | Trp | Pro | |
| 445 | | | | | | | | | | | | | | | 990 | | |
| 448 | Gln | Val | Leu | Gln | Asn | Ser | Met | Ala | Ala | Thr | Tyr | Glu | Asp | Arg | Gly | Pro | |
| 449 | | | | | | | | | | | | | | | 1005 | | |
| 452 | Ile | Gln | Asn | Phe | Arg | Ile | Glu | Met | Ser | Ile | Phe | Tyr | Ile | Val | Tyr | | |
| 453 | | 1010 | | | | 1015 | | | | | | | 1020 | | | | |
| 456 | Phe | Val | Val | Phe | Pro | Phe | Phe | Phe | Val | Asn | Ile | Phe | Val | Ala | Leu | | |
| 457 | | | | | | | | | | | | | | | 1035 | | |
| 460 | Ile | Ile | Ile | Thr | Phe | Gln | Glu | Gln | Gly | Glu | Ala | Glu | Leu | Gln | Asp | | |
| 461 | | | | | | | | | | | | | | | 1050 | | |
| 464 | Gly | Glu | Ile | Asp | Lys | Asn | Gln | Lys | Ser | Cys | Ile | Asp | Phe | Thr | Ile | | |
| 465 | | | | | | | | | | | | | | | 1065 | | |
| | 1055 | | | | 1060 | | | | | | | | | | | | |

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/534,279

DATE: 05/23/2006
TIME: 14:03:59

Input Set : A:\60290-USA Sequence Listing.txt
Output Set: N:\CRF4\05232006\J534279.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 35
Seq#:21; N Pos. 1
Seq#:22; N Pos. 25,31
Seq#:49; N Pos. 18,24
Seq#:65; N Pos. 27
Seq#:67; N Pos. 20
Seq#:77; N Pos. 15,18

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:19; Line(s) 3492

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42
Seq#:43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66
Seq#:67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83

VERIFICATION SUMMARY
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Input Set : A:\60290-USA Sequence Listing.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:3521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:3544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:0
L:3898 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:4109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0
L:4140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0
L:4276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:77 after pos.:0